Colloqui della Classe di Scienze

Anno Accademico 2021/2022

**Scuola Normale Superiore
Piazza dei Cavalieri, 7 - PISA**

3 NOVEMBRE 2021
ore 15.00

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Mathematical Virology: A Novel Perspective on Virus Structure, Assembly and Disassembly with Applications in Virus Nanotechnology

ABSTRACT:
Viral protein containers, called capsids, are repurposed for applications in virus nanotechnology, including gene therapy and vaccinology. These containers sit on a physico-chemical knife's edge: they must be sufficiently stable to provide protection for their cargoes, whilst facilitating their timely release in the viral life cycle upon cues from the host cell environment. In this talk, I will demonstrate that this delicate balance hinges on geometric properties of the capsid, that we classified via a generalised principle of quasi-equivalence. This theory contains the seminal Caspar Klug theory of virus architecture as a special case and provides geometric models for distinct capsid layouts in terms of Archimedean lattices. Based on these results, we demonstrated that a capsid's propensity to fragment, a proxy for its ease of disassembly and genome release, depends on two geometric/topological descriptors: its surface lattice type, and the interaction network between its tiles. Tiling models of viral capsids, and Hamiltonian paths associated with these geometric descriptors also provide a better understanding of virus assembly. This has been instrumental in the discovery of genome-encoded virus assembly instructions and has provided a means to better understand how this assembly mechanism works. We recently demonstrated that this mechanism also spontaneously evolved in a bacterial system that packages its own messenger RNA, resulting in increased packaging efficiency of the nucleic acid into its protein container. This highlights the wider importance of this assembly mechanism in biology and opens novel avenues for applications in virus nanotechnology and therapy.

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